

We claim:

1. A method for the fermentative production of at least one sulfur-containing fine chemical,
which comprises the following steps:
 - a) fermentation of a coryneform bacteria culture producing the desired sulfur-containing fine chemical, the coryneform bacteria expressing at least one heterologous nucleotide sequence which codes for a protein with O-acetylhomoserine sulfhydrolase (metY) activity;
 - b) concentration of the sulfur-containing fine chemical in the medium or in the bacterial cells, and
 - c) isolation of the sulfur-containing fine chemical.
2. A method as claimed in claim 1, wherein the sulfur-containing fine chemical comprises L-methionine.
3. A method as claimed in either of the preceding claims, wherein the heterologous metY-encoding nucleotide sequence is less than 100% homologous to the metY-encoding sequence from *Corynebacterium glutamicum* ATCC 13032.
4. A method as claimed in claim 3, wherein the metY-encoding sequence is derived from any of the following organisms:

<i>Corynebacterium diptheriae</i>	ATCC 14779
<i>Mycobacterium tuberculosis</i> CDC1551	ATCC 25584
<i>Clostridium acetobutylicum</i>	ATCC 824
<i>Bacillus halodurans</i>	ATCC21591
<i>Bacillus stearothermophilus</i>	ATCC 12980
<i>Chlorobium tepidum</i>	ATCC 49652
<i>Synechococcus</i> sp.	ATCC27104
<i>Emericella nidulans</i>	ATCC 36104
<i>Bacteroides fragilis</i>	ATCC 25285
<i>Lactococcus lactis</i>	ATCC 7962
<i>Bordetella bronchiseptica</i>	ATCC 19395
<i>Pseudomonas aeruginosa</i>	ATCC 17933
<i>Nitrosomonas europaea</i>	ATCC 19718
<i>Sinorhizobium meliloti</i>	ATCC 4399
<i>Thermotoga maritima</i>	ATCC 43589
<i>Streptococcus mutans</i>	ATCC 25175
<i>Burkholderia cepacia</i>	ATCC 25416

Deinococcus radiodurans	ATCC 13939
Rhodobacter capsulatus	ATCC 11166
Pasteurella multocida	ATCC 6530
Clostridium difficile	ATCC 9689
Campylobacter jejuni	ATCC 33560
Streptococcus pneumoniae	ATCC 6308
Saccharomyces cerevisiae	ATCC 2704
Kluyveromyces lactis	ATCC 8585
Candida albicans	ATCC 10231
Schizosaccharomyces pombe	ATCC 24969

5. A method as claimed in any of the preceding claims, wherein the metY-encoding sequence comprises a coding sequence according to SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51 and 53 or a nucleotide sequence homologous thereto which codes for a protein with metY activity.
6. A method as claimed in any of the preceding claims, wherein the metY-encoding sequence codes for a protein with metY activity, said protein comprising an amino acid sequence according to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52 and 54 or an amino acid sequence homologous thereto which represents a protein with metY activity.
7. A method as claimed in any of the preceding claims, wherein the coding metY sequence is a DNA or RNA which can be replicated in coryneform bacteria or is stably integrated into the chromosome.
8. A method as claimed in claim 7, wherein
 - a) a bacteria strain transformed with a plasmid vector carrying at least one copy of the coding metY sequence under the control of regulatory sequences is used, or
 - b) a strain in which the coding metY sequence has been integrated into the bacteria chromosome is used.
9. A method as claimed in any of the preceding claims, wherein the coding metY sequence is overexpressed.
10. A method as claimed in any of the preceding claims, wherein bacteria are fermented in

which additionally at least one further gene of the biosynthetic pathway of the desired sulfur-containing fine chemical has been amplified or mutated such that its activity is not influenced by metabolic metabolites.

- 5 11. A method as claimed in any of the preceding claims, wherein bacteria are fermented in which at least one metabolic pathway, which reduces the production of the desired sulfur-containing fine chemical, is at least partially switched off.
- 10 12. A method as claimed in any of the preceding claims, wherein coryneform bacteria are fermented in which, at the same time, at least one of the genes selected from among
- a) the gene *lysC*, which encodes an aspartate kinase,
 - b) the glyceraldehyde-3-phosphate dehydrogenase-encoding gene *gap*,
 - c) the 3-phosphoglycerate kinase-encoding gene *pgk*,
 - 15 d) the pyruvate carboxylase-encoding gene *pyc*,
 - e) the triose phosphate isomerase-encoding gene *tpi*,
 - f) the homoserine O-acetyltransferase-encoding gene *metA*,
 - g) the cystathionine gamma-synthase-encoding gene *metB*,
 - h) the cystathionine gamma-lyase-encoding gene *metC*,
 - 20 i) serine hydroxymethyltransferase-encoding gene *glyA*,
 - j) the methylene tetrahydrofolate reductase-encoding gene *metF*,
 - k) the vitamin B12-dependent methionine synthase-encoding gene *metH*,
 - l) the phosphoserine aminotransferase-encoding gene *serC*,
 - m) the phosphoserine phosphatase-encoding gene *serB*,
 - 25 n) the serine acetyltransferase-encoding gene *cysE*, and
 - o) the gene *hom*, which encodes a homoserine dehydrogenase,

is overexpressed or mutated in such a way that the activity of the corresponding proteins is influenced by metabolic metabolites to a smaller extent, if at all, compared to nonmutated proteins.

30

13. A method as claimed in any of the preceding claims, wherein coryneform bacteria are fermented in which, at the same time, at least one of the genes selected from among
- a) the homoserine kinase-encoding gene *thrB*,

- b) the threonine dehydratase-encoding gene *ilvA*,
- c) the threonine synthase-encoding gene *thrC*,
- d) the meso-diaminopimelate D-dehydrogenase-encoding gene *ddh*,
- e) the phosphoenolpyruvate carboxykinase-encoding gene *pck*,
- 5 f) the glucose-6-phosphate 6-isomerase-encoding gene *pgi*,
- g) the pyruvate oxidase-encoding gene *poxB*,
- h) the dihydrodipicolinate synthase-encoding gene *dapA*,
- i) the dihydrodipicolinate reductase-encoding gene *dapB*; and
- 10 j) the diaminopicolinate decarboxylase-encoding gene,

is attenuated by changing the rate of expression or by introducing a specific mutation.

14. A method as claimed in one or more of the preceding claims, wherein microorganisms of the species *Corynebacterium glutamicum* are used.

15. A method for producing an L-methionine-containing animal feed additive from fermentation broths, which comprises the following steps:

- a) culturing and fermentation of an L-methionine-producing microorganism in a fermentation medium;
- 20 b) removal of water from the L-methionine-containing fermentation broth;
- c) removal of from 0 to 100% by weight of the biomass formed during fermentation; and
- d) drying of the fermentation broth obtained according to b) and/or c), in order to obtain the animal feed additive in the desired powder or granule form.

16. A method as claimed in claim 15, wherein microorganisms according to the definition in any of claims 1 to 14 are used.